

# Raw Sequence Listing Error Summary

| <u>ERROR DETECTED</u>  | <u>SUGGESTED CORRECTION</u>  | <u>SERIAL NUMBER:</u> <u>09/643,755</u> |
|--|--|---|
| ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE |  |   |
| 1 <input type="checkbox"/> Wrapped Nuclecs   | The number/text at the end of each line "wrapped" down to the next line.<br>This may occur if your file was retrieved in a word processor after creating it.<br>Please adjust your right margin to .3, as this will prevent "wrapping".  |   |
| 2 <input type="checkbox"/> Wrapped Aminos  | The amino acid number/text at the end of each line "wrapped" down to the next line.<br>This may occur if your file was retrieved in a word processor after creating it.<br>Please adjust your right margin to .3, as this will prevent "wrapping".   |   |
| 3 <input type="checkbox"/> Incorrect Line Length   | The rules require that a line not exceed 72 characters in length. This includes spaces.  |   |
| 4 <input type="checkbox"/> Misaligned Amino Acid Numbering   | The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.  |   |
| 5 <input type="checkbox"/> Non-ASCII   | This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.<br>Please ensure your subsequent submission is saved in ASCII text so that it can be processed.  |   |
| 6 <input type="checkbox"/> Variable Length   | Sequence(s) <input type="checkbox"/> contain n's or Xaa's which represented more than one residue.<br>As per the rules, each n or Xaa can only represent a single residue.<br>Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.  |   |
| 7 <input type="checkbox"/> PatentIn ver. 2.0 "bug"   | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) <input type="checkbox"/> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.   |   |
| 8 <input type="checkbox"/> Skipped Sequences (OLD RULES)   | Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence:<br>(2) INFORMATION FOR SEQ ID NO:X:<br>(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")<br>(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:<br>This sequence is intentionally skipped<br><br>Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s). |   |
| 9 <input type="checkbox"/> Skipped Sequences (NEW RULES)   | Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence.<br><210> sequence id number<br><400> sequence id number<br>000  |   |
| 10 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)  | Use of n's and/or Xaa's have been detected in the Sequence Listing.<br>Use of <220> to <223> is MANDATORY if n's or Xaa's are present.<br>In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.   |   |
| 11 <input type="checkbox"/> Use of <213>Organism (NEW RULES)   | Sequence(s) <input type="checkbox"/> are missing this mandatory field or its response.   |   |
| 12 <input checked="" type="checkbox"/> Use of <220>Feature (NEW RULES)                               | #<br>Sequence(s) <u>4</u> are missing the <220>Feature and associated headings.<br>Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"<br>Please explain source of genetic material in <220> to <223> section.<br>(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)   |   |
| 13 <input type="checkbox"/> PatentIn ver. 2.0 "bug"  | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.   |   |

OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/643,755

DATE: 08/30/2000  
TIME: 14:32:19

Input Set : A:\Sequence  
Output Set: N:\CRF3\08302000\I643755.raw

Does Not Comply  
Corrected Diskette Needed

see p. 4, 6

```

4 <110> APPLICANT: van Rooijen, Gijs
5 Keon, Richard Glenn
6 Boothe, Joseph
7 Shen, Yin
10 <120> TITLE OF INVENTION: Commercial Production of Chymosin in Plants
12 <130> FILE REFERENCE: 9369-153
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/643,755
C--> 15 <141> CURRENT FILING DATE: 2000-08-23
17 <160> NUMBER OF SEQ ID NOS: 4
19 <170> SOFTWARE: PatentIn Ver. 2.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1173
23 <212> TYPE: DNA
24 <213> ORGANISM: Bovine
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (1)..(1173)
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33 1 5 10 15
35 caa tac ttc gtt gct gtt act cac gct gct gag atc acc acc cgc att cct 96
36 Gln Tyr Phe Val Ala Val Thr His Ala Ala Glu Ile Thr Arg Ile Pro
37 20 25 30
39 ctc tac aaa ggt aag tct ctc cgt aag gcg ctg aag gaa cat gga ctt 144
40 Leu Tyr Lys Gly Lys Ser Leu Arg Lys Ala Leu Lys Glu His Gly Leu
41 35 40 45
43 cta gaa gac ttc ttg cag aaa caa cag tat ggc atc agc agc aag tac 192
44 Leu Glu Asp Phe Leu Gln Lys Gln Tyr Gly Ile Ser Ser Lys Tyr
45 50 55 60
47 tcc ggc ttc ggt gaa gtt gct agc gtg cca ctt acc aac tac ctt gat 240
48 Ser Gly Phe Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp
49 65 70 75 80
51 agt caa tac ttt ggg aag atc tac ctc gga acc ccg cct caa gag ttc 288
52 Ser Gln Tyr Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe
53 85 90 95
55 acc gtt ctc ttt gat act ggt tcc tct gac ttc tgg gtt ccc tct atc 336
56 Thr Val Leu Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile
57 100 105 110
59 tac tgc aag agc aat gcc tgc aag aac cac caa aga ttc gat ccg aga 384
60 Tyr Cys Lys Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg
61 115 120 125
63 aag tcg tcc acc ttc cag aac tta ggc aaa ccc ttg tct ata cac tac 432
64 Lys Ser Ser Thr Phe Gln Asn Leu Gly Lys Pro Leu Ser Ile His Tyr
65 130 135 140
67 ggt aca ggt agc atg caa gga atc tta ggc tat gat acc gtc act gtc 480
68 Gly Thr Gly Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val

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TIME: 14:32:19

Input Set : A:\Sequence  
Output Set: N:\CRF3\08302000\I643755.raw

|     |   |     |     |     |      |
|-----|---|-----|-----|-----|------|
| 69  | 145   | 150 | 155 | 160 |      |
| 71  | tcc aac att gtg gac att caa cag aca gta gga ctt agc acc caa gaa |     |     |     | 528  |
| 72  | Ser Asn Ile Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu |     |     |     |      |
| 73  | 165   | 170 | 175 |     |      |
| 75  | cca ggt gat gtc ttc acc tat gca gaa ttc gat ggc atc ctt ggt atg |     |     |     | 576  |
| 76  | Pro Gly Asp Val Phe Thr Tyr Ala Glu Phe Asp Gly Ile Leu Gly Met |     |     |     |      |
| 77  | 180   | 185 | 190 |     |      |
| 79  | gca tac cca tcg ctc gcg tca gag tac tcg ata cct gtg ttt gac aac |     |     |     | 624  |
| 80  | Ala Tyr Pro Ser Leu Ala Ser Glu Tyr Ser Ile Pro Val Phe Asp Asn |     |     |     |      |
| 81  | 195   | 200 | 205 |     |      |
| 83  | atg atg aac cga cac cta gta gct caa gac ttg ttc tcg gtt tac atg |     |     |     | 672  |
| 84  | Met Met Asn Arg His Leu Val Ala Gln Asp Leu Phe Ser Val Tyr Met |     |     |     |      |
| 85  | 210   | 215 | 220 |     |      |
| 87  | gac agg aat ggc cag gag agc atg ctc acg ctt gga gct att gat cca |     |     |     | 720  |
| 88  | Asp Arg Asn Gly Gln Glu Ser Met Leu Thr Leu Gly Ala Ile Asp Pro |     |     |     |      |
| 89  | 225   | 230 | 235 | 240 |      |
| 91  | tcc tac tac aca gga tct ctt cac tgg gtt cca gtc act gtg cag cag |     |     |     | 768  |
| 92  | Ser Tyr Thr Gly Ser Leu His Trp Val Pro Val Thr Val Gln Gln     |     |     |     |      |
| 93  | 245   | 250 | 255 |     |      |
| 95  | tac tgg caa ttc act gtg gac agt gtc acc atc agc ggt gtg gtt     |     |     |     | 816  |
| 96  | Tyr Trp Gln Phe Thr Val Asp Ser Val Thr Ile Ser Gly Val Val Val |     |     |     |      |
| 97  | 260   | 265 | 270 |     |      |
| 99  | gca tgt gaa ggt gga tgt caa gct atc ttg gat acc ggt acg tcc aag |     |     |     | 864  |
| 100 | Ala Cys Glu Gly Gly Cys Gln Ala Ile Leu Asp Thr Gly Thr Ser Lys |     |     |     |      |
| 101 | 275   | 280 | 285 |     |      |
| 103 | ctg gtc gga cct agc agc gac att ctc aac att cag caa gct att gga |     |     |     | 912  |
| 104 | Leu Val Gly Pro Ser Ser Asp Ile Leu Asn Ile Gln Gln Ala Ile Gly |     |     |     |      |
| 105 | 290   | 295 | 300 |     |      |
| 107 | gcc aca cag aac cag tac ggt gag ttt gac ata gat tgc gac aac ctt |     |     |     | 960  |
| 108 | Ala Thr Gln Asn Gln Tyr Gly Glu Phe Asp Ile Asp Cys Asp Asn Leu |     |     |     |      |
| 109 | 305   | 310 | 315 | 320 |      |
| 111 | agc tac atg cct aca gtt gtc ttt gag atc aac ggc aag atg tac cca |     |     |     | 1008 |
| 112 | Ser Tyr Met Pro Thr Val Val Phe Glu Ile Asn Gly Lys Met Tyr Pro |     |     |     |      |
| 113 | 325   | 330 | 335 |     |      |
| 115 | ctg acc ccc tcc gcc tat acc agc cag gat caa ggg ttc tgc acc agt |     |     |     | 1056 |
| 116 | Leu Thr Pro Ser Ala Tyr Thr Ser Gln Asp Gln Gly Phe Cys Thr Ser |     |     |     |      |
| 117 | 340   | 345 | 350 |     |      |
| 119 | gga ttc cag agt gag aac cat tcc cag aaa tgg atc ttg gga gat gtg |     |     |     | 1104 |
| 120 | Gly Phe Gln Ser Glu Asn His Ser Gln Lys Trp Ile Leu Gly Asp Val |     |     |     |      |
| 121 | 355   | 360 | 365 |     |      |
| 123 | tcc att cgt gag tac tac agc gtc ttt gac agg gcc aac aac ctc gtt |     |     |     | 1152 |
| 124 | Phe Ile Arg Glu Tyr Tyr Ser Val Phe Asp Arg Ala Asn Asn Leu Val |     |     |     |      |
| 125 | 370   | 375 | 380 |     |      |
| 127 | ggg cta gct aaa gca atc tga                                     |     |     |     | 1173 |
| 128 | Gly Leu Ala Lys Ala Ile   |     |     |     |      |
| 129 | 385   | 390 |     |     |      |
| 132 | <210> SEQ ID NO: 2  |     |     |     |      |
| 133 | <211> LENGTH: 390   |     |     |     |      |
| 134 | <212> TYPE: PRT   |     |     |     |      |

RAW SEQUENCE LISTING  
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Input Set : A:\Sequence  
Output Set: N:\CRF3\08302000\I643755.raw

135 <213> ORGANISM: Bovine  
137 <400> SEQUENCE: 2  
138 Met Asn Phe Leu Lys Ser Phe Pro Phe Tyr Ala Phe Leu Cys Phe Gly  
139 1 5 10 15  
141 Gln Tyr Phe Val Ala Val Thr His Ala Ala Glu Ile Thr Arg Ile Pro  
142 20 25 30  
144 Leu Tyr Lys Gly Lys Ser Leu Arg Lys Ala Leu Lys Glu His Gly Leu  
145 35 40 45  
147 Leu Glu Asp Phe Leu Gln Lys Gln Gln Tyr Gly Ile Ser Ser Lys Tyr  
148 50 55 60  
150 Ser Gly Phe Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp  
151 65 70 75 80  
153 Ser Gln Tyr Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe  
154 85 90 95  
156 Thr Val Leu Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile  
157 100 105 110  
159 Tyr Cys Lys Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg  
160 115 120 125  
162 Lys Ser Ser Thr Phe Gln Asn Leu Gly Lys Pro Leu Ser Ile His Tyr  
163 130 135 140  
165 Gly Thr Gly Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val  
166 145 150 155 160  
168 Ser Asn Ile Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu  
169 165 170 175  
171 Pro Gly Asp Val Phe Thr Tyr Ala Glu Phe Asp Gly Ile Leu Gly Met  
172 180 185 190  
174 Ala Tyr Pro Ser Leu Ala Ser Glu Tyr Ser Ile Pro Val Phe Asp Asn  
175 195 200 205  
177 Met Met Asn Arg His Leu Val Ala Gln Asp Leu Phe Ser Val Tyr Met  
178 210 215 220  
180 Asp Arg Asn Gly Gln Glu Ser Met Leu Thr Leu Gly Ala Ile Asp Pro  
181 225 230 235 240  
183 Ser Tyr Tyr Thr Gly Ser Leu His Trp Val Pro Val Thr Val Gln Gln  
184 245 250 255  
186 Tyr Trp Gln Phe Thr Val Asp Ser Val Thr Ile Ser Gly Val Val Val  
187 260 265 270  
189 Ala Cys Glu Gly Gly Cys Gln Ala Ile Leu Asp Thr Gly Thr Ser Lys  
190 275 280 285  
192 Leu Val Gly Pro Ser Ser Asp Ile Leu Asn Ile Gln Gln Ala Ile Gly  
193 290 295 300  
195 Ala Thr Gln Asn Gln Tyr Gly Glu Phe Asp Ile Asp Cys Asp Asn Leu  
196 305 310 315 320  
198 Ser Tyr Met Pro Thr Val Val Phe Glu Ile Asn Gly Lys Met Tyr Pro  
199 325 330 335  
201 Leu Thr Pro Ser Ala Tyr Thr Ser Gln Asp Gln Gly Phe Cys Thr Ser  
202 340 345 350  
204 Gly Phe Gln Ser Glu Asn His Ser Gln Lys Trp Ile Leu Gly Asp Val  
205 355 360 365  
207 Phe Ile Arg Glu Tyr Tyr Ser Val Phe Asp Arg Ala Asn Asn Leu Val

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Output Set: N:\CRF3\08302000\I643755.raw

|     |  |      |     |
|-----|--|------|-----|
| 208 | 370  | 375  | 380 |
| 210 | Gly Leu Ala Lys Ala Ile  |      |     |
| 211 | 385  | 390  |     |
| 214 | <210> SEQ ID NO: 3   |      |     |
| 215 | <211> LENGTH: 3957   |      |     |
| 216 | <212> TYPE: DNA  |      |     |
| 217 | <213> ORGANISM: Artificial Sequence  |      |     |
| 219 | <220> FEATURE:   |      |     |
| 220 | <221> NAME/KEY: CDS  |      |     |
| 221 | <222> LOCATION: (1554)..(2726)   |      |     |
| 223 | <220> FEATURE:   |      |     |
| 224 | <223> OTHER INFORMATION: Description of Artificial Sequence, Figure 2      |      |     |
| 226 | <400> SEQUENCE: 3  |      |     |
| 227 | ctgcaggaaat tcattgtact cccagtatca ttatagtgaa agttttggot ctctcgccgg 60      |      |     |
| 229 | tggttttta cctcattta aagggtttt ccacccaaaa attctgttat catttcact 120          |      |     |
| 231 | ttacttgtta cttaatttc tcataatctt tggtgaaat tattcacgtt ccgcacacga 180        |      |     |
| 233 | tatccctaca aattttat ttgtttaaaa ttttcaacc gcataaaaaa ttatgaagtc 240         |      |     |
| 235 | cgtctatct ttaatgttagt ctaacatccc catattgaaa tatataattt acttaattt 300       |      |     |
| 237 | agcgttggta gaaacataa agatttttattt ttattttctt tcatataaat gttaatata 360      |      |     |
| 239 | caatataaac aaatttttttta cottaagaag gattttccat ttatattttt aaaaatata 420     |      |     |
| 241 | ttagtcaacc acgttaatctt ctaataataa agttgttca aaagaataaa 480                 |      |     |
| 243 | aatttaactt ctaatttttt ttatttcact gatcttaaag caacacccag tgacacaact 540      |      |     |
| 245 | agccattttt ttctttgaat aaaaaaatcc aatttattttt gtattttttatacaatga 600        |      |     |
| 247 | aaatttcacc aaacaatcat ttgttggatt tctgaagcaa gtcatgttat gcaaaatct 660       |      |     |
| 249 | ataatttcca ttggacacta cggaaatgaaatc tggatgtcg tttttacatg cgagacacat 720    |      |     |
| 251 | tttcttaaagt aattttataa atatgttacta tattcaagat ttcatatataa aaataactcaa 780  |      |     |
| 253 | tattacttct aaaaaattaa ttagatataa ttaaaatattt acttttttaa tttaagttt 840      |      |     |
| 255 | aatttgttcaa ttgttgcata ttgatttttattt attctactat gttttaaatgg tttttagat 900  |      |     |
| 257 | agtttaaagt aaataataatg aatgttagtag agttgttagag ttttacccca aaccataaac 960   |      |     |
| 259 | tataacattt atggtgact aattttcata tattttttat tgccttttacc tttttttttt 1020     |      |     |
| 261 | atgttaagtcc gtaactagaa ttacagtggg ttgcctatggc actctgtggt cttttttttc 1080   |      |     |
| 263 | atgcatgggt cttgcgcaag aaaaagacaa agaacaaga aaaaagacaa aacagagaga 1140      |      |     |
| 265 | caaaacccaa tcacacaacc aactcaaaattt agtcaactggc tgatcaagat cggccgcgtcc 1200 |      |     |
| 267 | atgtatgtct aatgtccat caagcaaca cgtgtttaac atgcacttta aatggctcac 1260       |      |     |
| 269 | ccatctcaac ccacacacaa acacattggc ttttttttca tcatcaccac aaccacctgt 1320     |      |     |
| 271 | atatattcat tctttccgc cacctcaattt ttttcaattt aacacacgtc aacctgcata 1380     |      |     |
| 273 | tgcgtgtcat cccatgccca aacttccatg catgttccaa ccaccccttc tctttatataa 1440    |      |     |
| 275 | tacccatataa tacctctaat atcaactact tttttcatca tccatccatc cagagtacta 1500    |      |     |
| 277 | ctactctact actataatac cccaaacccaa ctcattttca atactactct actatgt 1556       |      |     |
| 278 |  | Met  |     |
| 279 |  | 1    |     |
| 281 | aac ttc ctt aag tct ttc cct tac gct ttc ctt tgt ttc ggt caa                | 1604 |     |
| 282 | Asn Phe Leu Lys Ser Phe Pro Phe Tyr Ala Phe Leu Cys Phe Gln                |      |     |
| 283 | 5 10 15  |      |     |
| 285 | tac ttc gtt gct act cac gct gct gag atc acc cgc att cct ctc                | 1652 |     |
| 286 | Tyr Phe Val Ala Val Thr His Ala Ala Glu Ile Thr Arg Ile Pro Leu            |      |     |
| 287 | 20 25 30   |      |     |
| 289 | tac aaa ggt aag tct ctc cgt aag gcg ctg aag gaa cat gga ctt cta            | 1700 |     |
| 290 | Tyr Lys Gly Lys Ser Leu Arg Lys Ala Leu Lys Glu His Gly Leu Leu            |      |     |

More specific source of genetic material in the artificial sequence

See #12 on Error Summary Sheet.

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Input Set : A:\Sequence  
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|     |   |     |     |      |
|-----|---|-----|-----|------|
| 291 | 35  | 40  | 45  |      |
| 293 | gaa gac ttc ttg cag aaa caa cag tat ggc atc agc agc aag tac tcc     |     |     | 1748 |
| 294 | Glu Asp Phe Leu Gln Lys Gln Gln Tyr Gly Ile Ser Ser Lys Tyr Ser     |     |     |      |
| 295 | 50  | 55  | 60  | 65   |
| 297 | ggc ttc ggt gaa gtt gct agc gtg cca ctt acc aac tac ctt gat agt     |     |     | 1796 |
| 298 | Gly Phe Gly Glu Val Ala Ser Val Pro Leu Thr Asn Tyr Leu Asp Ser     |     |     |      |
| 299 | 70  | 75  | 80  |      |
| 301 | caa tac ttt ggg aag atc tac ctc gga acc ccg cct caa gag ttc acc     |     |     | 1844 |
| 302 | Gln Tyr Phe Gly Lys Ile Tyr Leu Gly Thr Pro Pro Gln Glu Phe Thr     |     |     |      |
| 303 | 85  | 90  | 95  |      |
| 305 | gtt ctc ttt gat act ggt tcc tct gac ttc tgg gtt ccc tct atc tac     |     |     | 1892 |
| 306 | 306 Val Leu Phe Asp Thr Gly Ser Ser Asp Phe Trp Val Pro Ser Ile Tyr |     |     |      |
| 307 | 100   | 105 | 110 |      |
| 309 | tgc aag agc aat gcc tgc aag aac cac caa aga ttc gat ccg aga aag     |     |     | 1940 |
| 310 | Cys Lys Ser Asn Ala Cys Lys Asn His Gln Arg Phe Asp Pro Arg Lys     |     |     |      |
| 311 | 115   | 120 | 125 |      |
| 313 | tcg tcc acc ttc cag aac tta ggc aaa ccc ttg tct ata cac tac ggt     |     |     | 1988 |
| 314 | Ser Ser Thr Phe Gln Asn Leu Gly Lys Pro Leu Ser Ile His Tyr Gly     |     |     |      |
| 315 | 130   | 135 | 140 | 145  |
| 317 | aca ggt agc atg caa gga atc tta ggc tat gat acc gtc act gtc tcc     |     |     | 2036 |
| 318 | Thr Gly Ser Met Gln Gly Ile Leu Gly Tyr Asp Thr Val Thr Val Ser     |     |     |      |
| 319 | 150   | 155 | 160 |      |
| 321 | aac att gtg gac att caa cag aca gta gga ctt agc acc caa gaa cca     |     |     | 2084 |
| 322 | Asn Ile Val Asp Ile Gln Gln Thr Val Gly Leu Ser Thr Gln Glu Pro     |     |     |      |
| 323 | 165   | 170 | 175 |      |
| 325 | ggt gat gtc ttc acc tat gca gaa ttc gat ggc atc ctt ggt atg gca     |     |     | 2132 |
| 326 | Gly Asp Val Phe Thr Tyr Ala Glu Phe Asp Gly Ile Leu Gly Met Ala     |     |     |      |
| 327 | 180   | 185 | 190 |      |
| 329 | tac cca tcg ctc gcg tca gag tac tcg ata cct gtg ttt gac aac atg     |     |     | 2180 |
| 330 | Tyr Pro Ser Leu Ala Ser Glu Tyr Ser Ile Pro Val Phe Asp Asn Met     |     |     |      |
| 331 | 195   | 200 | 205 |      |
| 333 | atg aac cga cac cta gta gct caa gac ttg ttc tcg gtt tac atg gac     |     |     | 2228 |
| 334 | Met Asn Arg His Leu Val Ala Gln Asp Leu Phe Ser Val Tyr Met Asp     |     |     |      |
| 335 | 210   | 215 | 220 | 225  |
| 337 | agg aat ggc cag gag agc atg ctc acg ctt gga gct att gat cca tcc     |     |     | 2276 |
| 338 | Arg Asn Gly Gln Glu Ser Met Leu Thr Leu Gly Ala Ile Asp Pro Ser     |     |     |      |
| 339 | 230   | 235 | 240 |      |
| 341 | tac tac aca gga tct ctt cac tgg gtt cca gtc act gtg cag cag tac     |     |     | 2324 |
| 342 | Tyr Tyr Thr Gly Ser Leu His Trp Val Pro Val Thr Val Gln Gln Tyr     |     |     |      |
| 343 | 245   | 250 | 255 |      |
| 345 | tgg caa ttc act gtg gac agt gtc acc atc agc ggt gtg gtt gca         |     |     | 2372 |
| 346 | Trp Gln Phe Thr Val Asp Ser Val Thr Ile Ser Gly Val Val Val Ala     |     |     |      |
| 347 | 260   | 265 | 270 |      |
| 349 | tgt gaa ggt gga tgt caa gct atc ttg gat acc ggt acg tcc aag ctg     |     |     | 2420 |
| 350 | Cys Glu Gly Gly Cys Gln Ala Ile Leu Asp Thr Gly Thr Ser Lys Leu     |     |     |      |
| 351 | 275   | 280 | 285 |      |
| 353 | gtc gga cct agc agc gac att ctc aac att cag caa gct att gga gcc     |     |     | 2468 |
| 354 | Val Gly Pro Ser Ser Asp Ile Leu Asn Ile Gln Gln Ala Ile Gly Ala     |     |     |      |
| 355 | 290   | 295 | 300 | 305  |

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P. 6

Missing mandatory <220> and  
<223> features to explain  
artificial sequence. See #12  
on Error Summary Sheet.

<210> 4

<211> 390

<212> PRT

<213> Artificial Sequence

<400> 4

Met Asn Phe Leu Lys Ser Phe Pro Phe Tyr Ala Phe Leu Cys Phe Gly

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/643,755

DATE: 08/30/2000  
TIME: 14:32:20

Input Set : A:\Sequence  
Output Set: N:\CRF3\08302000\I643755.raw

L:14 M:270 C: Current Application Number differs, Replaced Application Number  
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:429 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:429 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: